Small Mammal Sampling Protocol for Long-term Ecological Monitoring Program Denali National Park and Preserve

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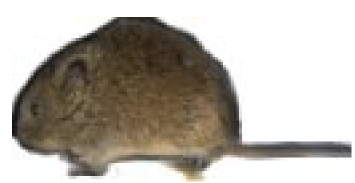

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Denali Small mammal monitoring protocol

1. Objectives

a. Species of interest

The small mammal investigations begun in the Rock Cr. watershed of Denali National Park and Preserve in 1992 focused primarily on three species: the northern red-backed vole (*Clethrionomys rutilus*), the tundra vole (*Microtus oeconomus*), and the singing vole (*Microtus miurus*). Captures were also recorded of northern bog lemmings (*Synaptomys borealis)* and shrews (*Sorex spp.*), but demographic information was not collected on these species.

b. Measure abundance/density

Two competing trapping methods were employed for the assessment of population changes over time. Trapping grids, described by Otis et al. (1978), are used primarily for the estimation of population abundance, but are adaptable for the estimation of density. With traps in a grid configuration, traps are placed uniform distances apart in lines separated by the same distance as traps within a line, forming a rectangular trap pattern.

Trapping webs, described by Wilson and Anderson (1985), employ distance sampling theory, and are primarily used for the direct estimation of density, but may also be used for the estimation of abundance. The trap configuration uses traps placed in concentric rings, a fixed distance apart. Each ring contains a fixed number of traps, and as a consequence, the distance between traps within a ring increases as distance from the center of the web increases.

c. Assess demographic processes

Repeated sampling of the study plots during the snowfree period allowed assessment not only of population abundance and density, but also a determination of demographic processes acting on the populations between sampling occasions. Additions to the populations, either through reproduction or immigration could be estimated between sampling occasions. Similarly apparent survival rate (which includes emigration that cannot be separately estimated from mortality) can also be determined. These measures provide additional insight into the processes that give rise to the state of the population at the time of the sampling occasion.

2. Sampling approach

Animals were captured using livetrapping techniques because of the need to maintain sampling for an indefinite length of time as part of a monitoring program. Removal sampling, where animals are removed by snap traps or pitfall traps, has a demonstrable effect upon the population being monitored. This is a biological example of the Heisenberg Uncertainty Principle, in which the phenomenon being observed is altered through the process of observation.

Sampling plots were placed in the watershed with a scheme intended to produce abundance estimates representative of the entire watershed. Plots were placed in the riparian zone of the watershed, where the width of the riparian zone was sufficient to accommodate a sample plot. Sample plots were also placed in the open canopy/shrub habitats on the benches of the watershed where the topography was not too extreme for human locomotion.

Within these habitat types, replicate plots were placed to ensure that abundance measured in a plot was not an artefact of the plot location, but rather indicative of the habitat. The riparian zone was limiting in size such that only two replicates were placed in the habitat. The open canopy/shrub habitat was in greater abundance, so efforts were made to place plots on both east-facing and west-facing slopes.

Comparisons were made of abundance among plots within habitat types, and among plots between habitat types. The first comparisons measured whether plots were indeed replicates of the habitat types, and the second comparison examined habitat-specific demography, i.e., whether the source-sink theory of Pulliam (1988) was operative in the Rock Cr. watershed.

3. Personnel requirements

a. Staffing

Checking of traps requires a minimum of 2 people for each trap checked. This is particularly acute when animals need to be injected with PIT tags. One person is responsible for restraining the animal, while the other administers the tag. The configuration of study plots in the Rock Cr. watershed allowed the field crew to split into 2 teams. One member of the team was an experienced researcher, versed in the injection of tags and the identification of species and sexual characteristics. For the 700 traps used in Rock Cr. this equated to a minimum staffing of 4 individuals in camp at all times. Pairing of researchers was also a safety consideration, as should anyone be injured during the trap checks, there was a member of the crew available to give aide.

b. Species identification

All members of the field crew require a minimum of training in identification of species likely encountered in the field. Basic training can be achieved through examination of museum specimens; with substantial additional experience derived in the field under the supervision of trained staff members.

Defining characteristics of *Clethrionomys* is sharpness of the snout and exposure of ears. Differentiating characteristics between *M. oeconomus* and *M. miurus*: *M. miurus* is lighter in coloration (with golden sides) and a shorter, more blunt tail. *M. oeconomus* has a long, tapered tail dark on top and light on bottom. Lemmings have tails no longer than the hind foot and have grooved incisors. Differentiation between shrews, *S. cinerius* and *S. monticolus* is achieved only by examination of dentition with a handlens.

c. Stamina

As with any field work, small mammal trapping requires a substantial amount of physical exertion. Deploying 700 traps requires transporting approximately 350kg of traps into the field. This is in addition to tents, tarps, sleeping bags, cooking gear, food, personal gear, and processing equipment. Hours are long (0530-2230) and weather conditions are often uncomfortable.

With the sampling regimen we employ, and the configuration of sampling plots, approximately 7.5km are covered during each trap check. These checks are made 3 times day^{-1}, resulting in 22.5km traveled per day for 5 days. Splitting this in half because the crew splits trap responsibilities for each check, each member of the crew travels over 11km day^{-1}. In addition to this, multiple trips into and out of field camp are required to establish, break down, and provision camp. In English units, a crew member should be expected to travel roughly 40 miles in difficult terrain during the course of a 5-day sampling bout. As a result, crew members need to be in reasonably good physical condition.

4. Equipment

a. Traps

Traps used in the capture of animals for small mammal monitoring are manufactured by the H. B. Sherman Company. The size used is 7.6cm x 8.9cm x 22.9cm. This is sufficient to catch the largest lemming, while also having sufficient sensitivity to capture shrews. Prices of traps vary considerably, but can be acquired for $12-$16 each plus shipping.

To minimize thermal stress while animals are in traps, bedding material is placed inside traps. This is compressed cotton, formed into 6cm x 6cm x 1cm squares that can be shredded by animals into nests upon capture. These can be acquired from animal supply outlets.

For simplified handling of animals during processing, 1 gallon Ziploc plastic bags work quite well.

Each crew member carries at least 2 bags during checking: one bag for holding animals, and the other for transferring trash (soiled bedding material and feces) from the trap. Bags can be reused for several checks, but are changed daily because of soiling. In a typical week, roughly 100 bags are used.


Figure 2. Weighing captured animals.

Weighing of captured animals is done with 100g x 1g Pesola scales. These are clipped onto the Ziploc bags while the animal is inside, and the bag is re-weighed after the animal is released (Figure 1). The price is roughly $40 and each crew member is provided with a scale.

b. Marking technique

The use of passive integrated transponders has greatly simplified the marking process for small mammals. The chip, encased in glass, weighs 1g, and has external dimensions of 11mm x 2.1mm and has been successfully implanted, with the use of a 12-gauge needle, into animals as small as 8g. These tags are available from BioMark, Boise ID for roughly $5/tag.

Injection of tags consists of submerging the needle in iodine, inserting a tag into the needle, placing a dab of Betadine onto the end of the needle, scanning the tag with a tag reader to make sure it functions properly, and injecting the tag into the animal under the skin on the dorsal side near the shoulder blades. The Betadine is inserted into the puncture along with the tag, serving to minimize the possibility of infection. With fingers, the researcher moves the injected tag away from the puncture to ensure it does not work its way back out of the animal. Before the animal is released, the tag is scanned


Figure 3. PIT tag injection.

again, and tactile reinforcement makes sure the tag is properly seated in the animal (Figure 2).

PIT tags offer the advantage over ear tags and toe clipping of being difficult to lose, and easy to record. Voles groom themselves vigorously, and consequently are susceptible to losing ear tags. Placing PIT tags near the shoulder blades makes grooming of that location difficult.

Similarly detecting a marked animal is greatly simplified through the use of PIT tag readers. As 10-second scan while an animal is in a plastic bag will determine if it has been previously marked (Figure 3). Furthermore, the animal ID code is permanently stored in scanner memory at that time. In contrast, to determine the identity of an individual marked with toe-clipping, the animal must be removed from the plastic bag, held while examining each foot, while attempting to determine if a toe has been clipped or is merely short, finally, this pattern must be translated into a numeric code from the master records at camp.

Figure 4. Scanning for PIT tag after injection.

Processing time of an animal marked with a PIT tag is approximately 45 seconds from the time it is removed from the trap, weighed, scanned, and released. The animal is never handled by the crew member unless sexual characteristics need to be determined. In another minute the trap is reset, and the crew member is en route to the next trap. Conversely, checking the animal for missing appendages requires removing the animal from the bag and examining each foot; a process that requires no less than 2 minutes. Although the difference in time seems small, when this process is repeated 1500 times during the course of a trapping bout, the time savings are substantial.

c. Camp supplies

Establishment of a field camp for small mammal monitoring is no different than any other backcountry camp. Adequate consideration must be given to establishment of cooking sites, food storage, and latrine sites. An added consideration for small mammal work is the storage of sunflower seed bait and trap mortalities in bear-proof storage while in camp.

d. Refurbishing equipment at conclusion of field season

All field supplies must be adequately maintained during the field season, and particular care taken at the conclusion of the field season. This includes checking computers and Pesolas for proper functioning; replacing lost parts if necessary. The tag scanners suffer heavy use during the field season, and those scanners that have rechargeable batteries should have the batteries replaced at least every other field season. This can be done by the manufacturer, Destron-Fearing of St. Paul MN. Price of refurbishment is roughly $200. The economics of refurbishment become clouded by the fact that new scanners with replaceable batteries can be purchased for $500.

5. Training

a. Species identification

Training of the field crew in species identification should include one afternoon spent examining museum specimens to gain general familiarity with gross morphology, and the lion's share of the experience identifying species will come from hands-on work in the field, under the guidance of trained personnel.

b. Data entry

All personnel should be acquainted with the summary form of data recorded at each capture.

Date	Hr	Plot	X	Y	Tag#	N/R	Spec	Sex	Wt	Comments
08/05/96	6	FWE	8	B			SOSP			
08/05/96	6	FWE	11	B	4103742517	N	CLRU	M	13	

Figure 5. First 2 lines of a spreadsheet file showing data as entered in the field.

This will expedite communicating that information, in its proper order while on the study plots. A simple spreadsheet is used to record data in the field, and all personnel should be acquainted with use of the spreadsheet to add versatility to the crew composition.

c. Trap maintenance

It is fundamental that traps be in proper working order when on the study plots. Traps can fail to work for a variety of reasons: brush in trap, soiled trap, mechanically deformed in transit. It is important that traps be examined during their use to ensure these features are not present in the traps. Periodically during checking the traps, unoccupied traps should be sprung, to make sure they function. Over the course of the field season, traps should be dismantled and scrubbed to remove soil and feces from them. At the conclusion of the field season, traps should also be dismantled, cleaned and disinfected in preparation for the following field season.

6. Field procedures

a. Plot configuration

Protocol development has experimented with both trapping grids (rectangular) and trapping webs (circular). Based upon 3 field seasons employing both methods, I recommend discontinuation of trapping webs, and continued reliance upon trapping grids.

This decision is based upon the continued violation of the assumption of high detection probability at the center of a trapping web. Continual use of trapping webs for monitoring invariably leads to large amounts of foot traffic on the webs. Given the perpetual damp conditions of the plots during the field season, the vegetation becomes degraded. As a result, probability of capture at the center of webs diminishes as escape cover becomes scarce. The diminution of capture probability stipulated by distance sampling methods fails to take place; conversely, more detections take place at the edges of the webs than at the center. Fitting a monotonically decreasing function to data of this sort, leads to models that predict capture probability is constant across the web, which is patently false.

Using rectangular grids, other issues regarding trap placement involves the spacing of the traps. Traps should be placed no more than 10m apart to prevent animals from residing on the plots, but not encountering traps. This is particularly acute for female voles, whose movements are largely restricted during the field season because of maternal care devoted to young. The number of traps per grid should be governed by a rule-of-thumb calculation regarding sample size. To produce estimates of abundance and survival with adequate precision to detect change, approximately 50 individuals should be captured. With some a priori knowledge of the density of animals inhabiting particular locales, the areal extent of the grid can be approximated. For example, if the true population size is 100 animals ha^{-1}, and the probability of capture of individuals (probability an individual is captured given the animal resides on the plot) is roughly 0.25, then the size of a trapping grid should be approximately 2ha. If the grid is to be square, that implies a length of 141m, and if trap spacing is 10m, then a 15x15 grid of traps can be used. Similar calculations could be carried out for other densities, capture probabilities, and grid orientations (see also White et al. 1982).

Finally, with multiple, replicate grids within habitats, to employ an empirical measure of within habitat variation in demography, the spacing of grids must be considered. Mixing of individuals between grids invalidates the independence assumption necessary for the empirical measure of variation, so efforts should be made to space grids at distances sufficient such that

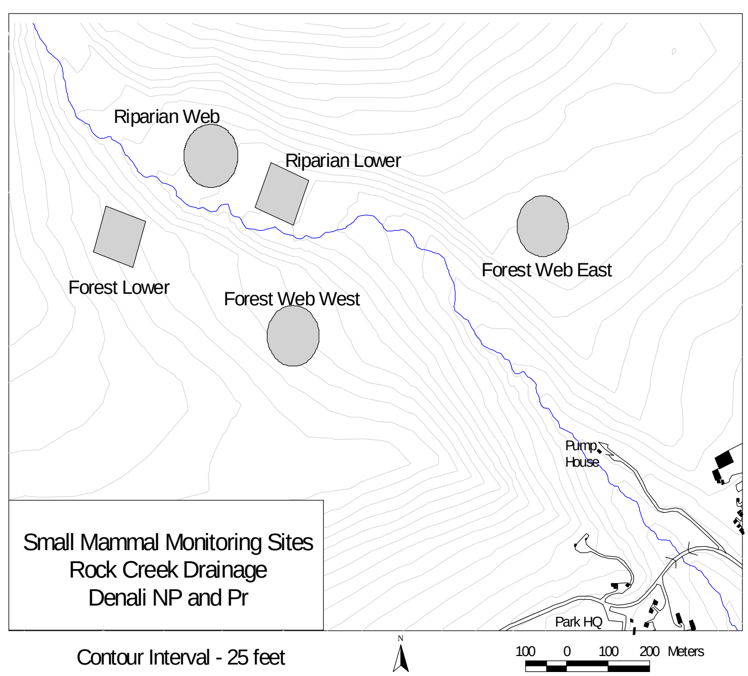

Figure 6. Small mammal sample plot configuration in Rock Cr. watershed.

animals are unlikely to traverse distances between grids. Telemetry data suggest northern red-backed voles are capable of traveling 250m in 10 hours. Consequently, if plausible, plots should be situated no closer than 500m. However, the drawback to this is the increase in travel time of the field crew between plots (Figure 5).

b. Sampling session duration

Within a sampling bout, the objective is to produce a precise estimate of population abundance. Using mark-recapture techniques, this objective is achieved by simultaneously capturing and marking a sufficient number of individuals, plus recapturing a sufficient fraction of the marked individuals to detect temporal, behavioral, or individual forms of heterogeneity in capture probabilities. Therefore, a sufficient number of capture occasions should take place to allow estimation of these quantities.

There is a danger, however, in having too many capture events. There is the physiological risk that animals subject to repeated confinement in traps, even though brief individually, may be too extensive in aggregate. This may cause weight loss because of lost foraging time in males, and possibly neonatal mortality because of lost attentiveness in maternal females. Indexes of this physiological stress can be measured using weight at capture to assess lost foraging time.

An additional danger in having trapping events extend over extended periods is the possible violation of the assumption of closure in the closed abundance estimation models. Closure means the population size does not change during the period of investigation. This assumption is tenable, i.e., it is roughly true, if the period during which births and deaths are assumed to be zero, is sufficiently short. Reviewing data from the past 5 years, it appears this assumption holds through a 4-day trapping session, but begins to break down on day 5.

To minimize stress to the animals associate with confinement, traps should be checked continuously. However, this imposes 2 difficulties. First, it becomes impossible to identify a sampling occasion, upon which mark-recapture models are premised. Second, this is an unreasonable expectation to place upon a field crew which needs rest to replenish their own nutrient reserves. Checking traps often results in traps working more efficiently; i.e., a single trap can catch more animals if it is emptied frequently. However, to allow sufficient time for the field crew to re-energize, a compromise of checking traps 3 times a day has been used. The first check of the day is at 0600; the second at 1400, and the third at 2000. This implies the maximum duration between checks is 10 hours. Near the end of the field season, this interval becomes somewhat longer because diminishing daylight requires beginning the evening check prior to 2000 so it can be finished before navigation between traps becomes impossible.

c. Sampling intensity during the field season

With the added objective of the monitoring protocol being to estimate survival and recruitment of individuals between sampling sessions, a combination of open and closed estimation models is used. (Figure 6) This "robust design" (Pollock et al. 1990) allows use of data from within session

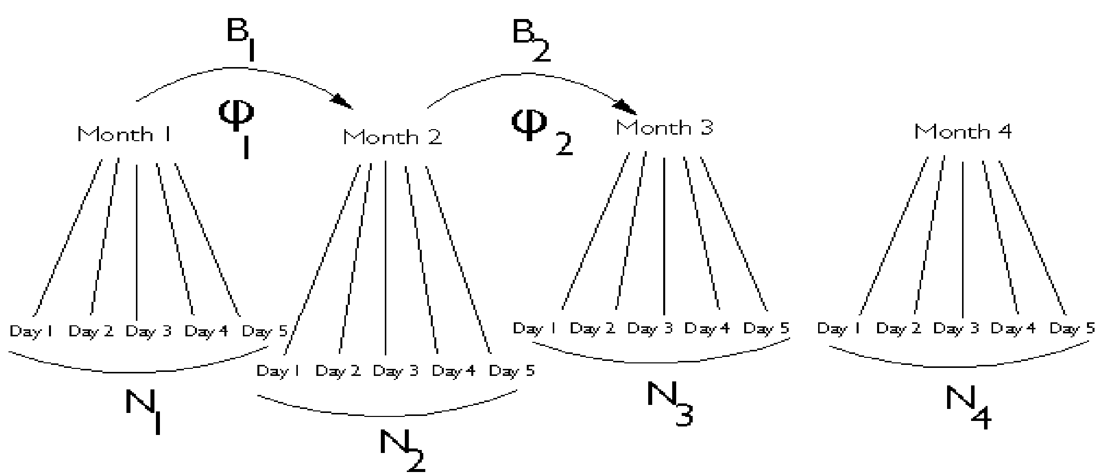

Figure 7. Diagram of robust design showing major and minor sampling occasions, and estimable parameters.

trapping to be used in the estimation of both abundance and survival/recruitment.

Substantial changes take place in small mammal populations during the snow-free season in DNPP. For the purposes of monitoring, it is important to know the demographic processes that give rise to those changes. Population increase can be brought about as a result of high survival and poor recruitment, or conversely, from low survival and high recruitment. Coupling the estimation of survival and recruitment with the measurement of abundance allows the contributing factors to abundance to be estimated.

The estimation of survival/recruitment requires data from both end-points of the interval of interest. However, using traditional Jolly-Seber estimation techniques, the presence of a marked individual in sampling occasion *k* is a result of 2 physical processes: surviving the period *k-1* to *k* (φ_{k-1}) <u>and</u> being captured on occasion *k* (p_k). As a result, these 2 parameters are not separately estimable under a time-specific Jolly-Seber model. The robust design alleviates this difficulty to some extent, but at the cost of alternative assumptions.

Consequently, to produce estimates of survival/recruitment, 2 more sampling sessions are required than the number of survival/recruitment estimates desired. Because survival late in the snow-free period is particularly critical to determining the state of the population the following spring, the sampling schedule should be designed such that the final sampling occasion takes place near the first snowfall.

d. Trap mortalities

Inevitably, some losses result from the trapping process, even though livetraps are used. Mortalities should be placed in individual plastic bags (sandwich bags work well) immediately after removal from traps. Information should be recorded and placed inside the bag upon return to field camp: species, sex, weight, date, time, trap location, plot, latitude, and longitude. As soon as practical, specimens should be frozen, and transported to the UA Museum for dissection and preservation.

Levels of contaminants, such as heavy metals, can be determined from body tissue. In addition, genetic information, such as genetic anomalies, and maternal/paternal characteristics can be determined from genetic analysis by the staff at the UA Museum. These specimens also provide archival information relating to the identification of species in the field. Differentiation between the shrew species is also only accomplished by study of dentition from trap mortalities.

7. Data storage

Recording data in electronic form as close to the time the data are available is fundamental to minimizing data errors. The problem of data entry errors is particularly acute when working with live animals that may not be resighted upon release. To compound this problem, the magnitude of data collected in a small mammal study is indeed voluminous. As an example, during the 1995 field season, 6622 individuals were removed from traps; including non-target species such as grey jays and red squirrels. Consequently, an efficient method of data entry needs to be employed not only to reduce entry errors, but also to process data in a timely fashion.

We use palmtop computers (16cm x 8.6cm x 2.5cm, 300g) manufactured by Hewlett-Packard to take to the traps. In this manner, data can be recorded electronically while the animal is still in-hand. The data are entered into a standard Lotus spreadsheet for easy transfer to desktop machines for subsequent analysis. PIT tag information is also stored in the scanners, and can be transferred to desktop machines for checking against the possibility of transcription errors.

While in field camp, data are transferred each evening from the palmtops to a laptop computer kept in camp. Data are saved to the hard disk and also to floppy disk, so that at the conclusion of each day in the field, data are stored in 3 locations. This has effectively eliminated our use of written notes for data collection; the single exception to this is the tags stored with the incidental mortalities (Figure 7).

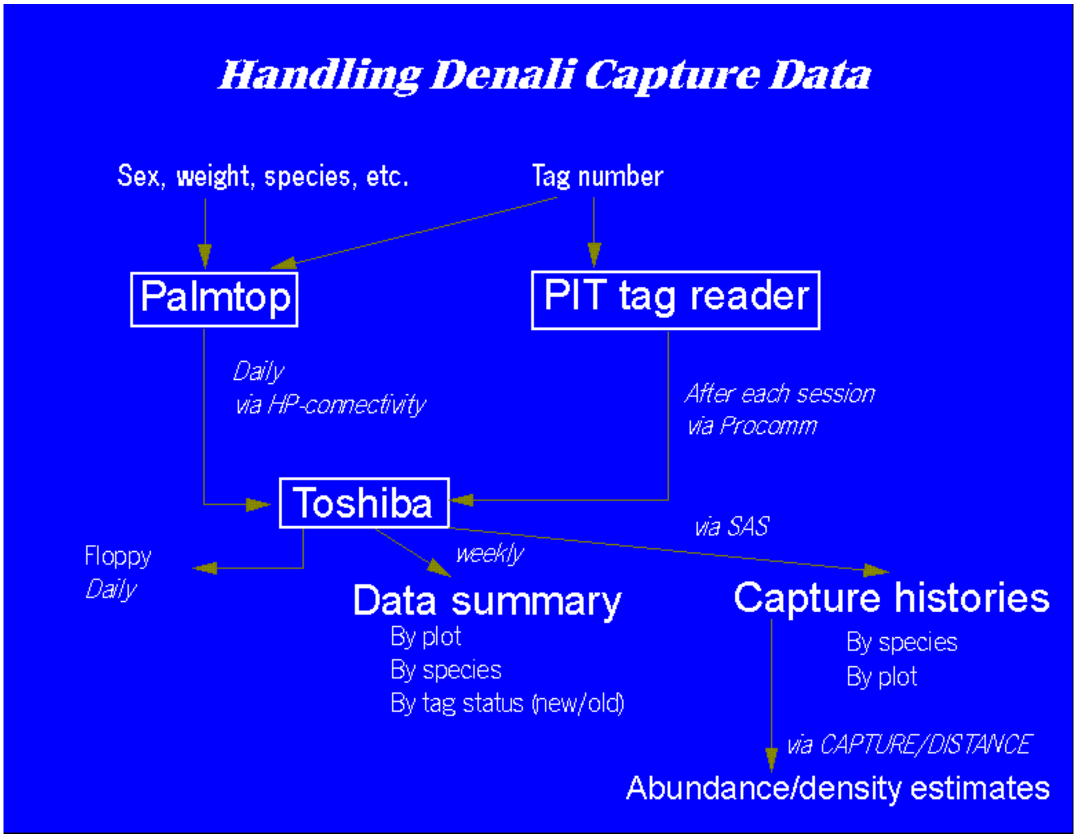

Figure 8. Flow of data, and data handling in the field for small mammal monitoring.

8. Data analysis

After the data have been collected and computerized in the field, they should be ready for analysis to estimate the demographic parameters of interest. However, given the volume of data, described above, several levels of error checking are employed prior to final analysis.

At the most rudimentary level, the data are sorted by tag number and obvious outliers can be noted by numbers appearing out of sequence. At a secondary level, a catalog of tags taken to the field can be checked against tags appearing in data files; tag numbers not appearing in the catalog are obviously in error. As a final step, capture histories (see below) are created using computer code described later. These data summaries are examined for anomalies such as this:

4142006A2C 0101101101

4142006C2A 0000010000

obviously indicating an error in the second tag number, which was only detected once, while a vary similar tag number was encountered very often, but not on the occasion when the trap-happy individual was missed.

The raw data entered in spreadsheet format, must be summarized into capture history format for estimation of demographic parameters. This consists of finding all trapping occasions on which an individual was encountered, noting the occasion of interest, entering a '1' in the capture history sequence, and filling the remainder of the sequence with '0'. In addition, data are stratified by species, sex, and plot because demographic parameters should be estimated for each of these categories individually. This is accomplished by the accompanying SAS program (Appendix I) after the data have been transformed from spreadsheet to dBASE format.

The SAS code not only converts the raw data to capture histories, but also inserts header information so that manufactured files can be directly submitted to program CAPTURE (Otis et al. 1978, Rexstad and Burnham 1991) for computation of abundance estimates. This program produces not only estimates of abundance, but also assesses the model most appropriate for the data being analyzed; determining the forms of variation in capture probabilities present in the data. Additionally, a statistical test of closure is also performed and reported by the program. This aids in the interpretation of the appropriateness of closed population models for the data of interest.

Program CAPTURE is also capable of producing estimates of density, using the method of nested grids (Otis et al. 1978). Furtsch (1995) found this to be a plausible method of estimation when adequate data were available, but in years of low vole abundance, this technique failed for lack of data.

Alternatively, CAPTURE computes the mean maximum distance moved (MMDM) for individuals in a data set. This is accomplished by using the Euclidean distance formula to compute distances between trap locations at which individuals are captured. The maximum of this distance for each individual is assumed to approximate the width of an individual's home range. The average of this value is computed across all animals in the data set. One half MMDM is then used as the width of a boundary strip (Dice 1938) which is added to the dimension of the trapping grid to produce the effective area of the trapping grid. Density of animals is produced by taking the abundance estimate ($\hat{N}$) and dividing by the effective area. Furtsch (1995) carried out these calculations, along with their associated measures of precision for DNPP data.

A substantially different approach to density estimation can be employed with data from the trapping webs. This theory, distance sampling theory, is described in Buckland et al. (1993); and program DISTANCE (Laake et al. 1993) computes the density estimates. Abundance is not estimated directly, but the spatial pattern of captures is used to estimate detection probability, which is in turn used to estimate density. This is exactly equivalent to the use of variable circular plots for estimation of density in passerines. Because of difficulties associated with data collection on trapping webs (discussed above), details of this analysis will not be presented.

Open population models (Pollock et al. 1990) are used for the estimation of survival and recruitment. Capture histories produced for use with closed population models are collapsed further to indicate whether an individual is detected at any time during the trapping session. These capture histories are analyzed by program JOLLY for parameter estimation. Goodness-of-fit tests are computed, and a series of models, with decreasing amounts of time-specificity in survival and recapture probabilities are fit to the data.

From the point estimates and associated standard errors, statistical comparisons of any demographic parameter estimates can be made. This was employed by Rexstad (1994) to test for differences in abundance between habitats and between years of the DNPP study. Similar comparisons could be made for survival and recruitment estimates, although recruitment estimates have notoriously large standard errors.

9. Integration with overall monitoring framework

a. Use of data from other monitoring components

Monitoring consists of activities beyond watching a system for indications of change. Understanding mechanisms responsible for changes is an important component of documenting the sources of intrinsic variation in ecosystem attributes. A large-scale monitoring program should also be integrative; i.e., coalescence of data from several components.

The pattern of good years/poor years in vole abundance may be explained by differences in winter conditions. A benign winter environment for nonhibernating voles involves a combination of timing, temperature, and snow depth. Meteorological conditions operate at quite small geographical scales, particularly in the Alaska Range. Consequently, meteorological data from the weather stations located in the Rock Cr. watershed would be beneficial to investigate local-scale differences in overwinter conditions.

Vegetative data, including berry production data, may be informative in measuring factors influencing survival and reproduction. A highly significant correlation of berry crop to vole abundance has been shown by Johnson

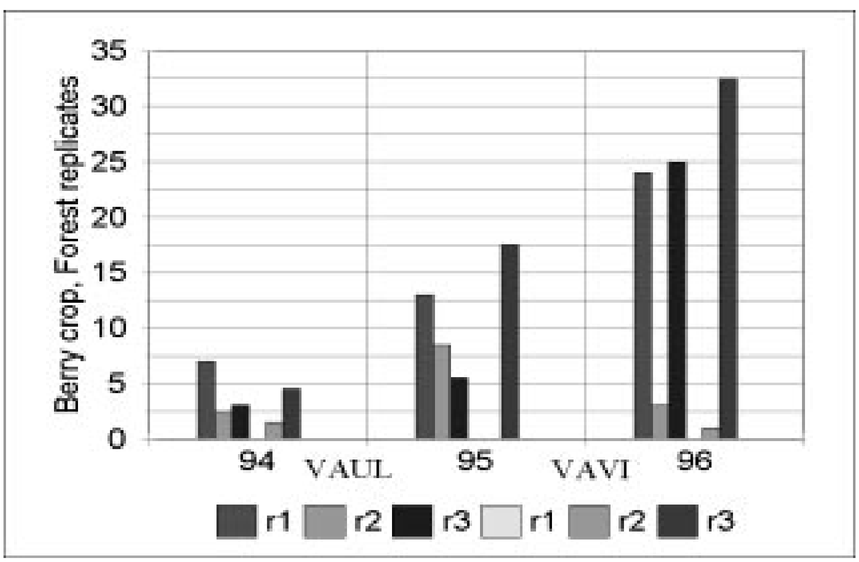

Figure 9. Berry production data from Rock Cr. forest vegetation plot.

et al. (1995) in Interior Alaska. Preliminary examination of berry production data leads to equivocal results about annual variation in berry crop (Figure 8). Careful thought should be given to the way in which berry crop influences vole demographics. Berries provide a food source for voles not only when they ripen in August, but through the remainder of that season, plus under the snow during the winter, and during green-up the following spring. Possibly a measure of persistence of berries beyond their production may be a better predictor of beneficial effects of berries on vole population dynamics.

Voles have also served as surrogate samplers to complement the fungal inventory in DNPP. Fecal samples from captured voles have been analyzed by Dr. Gary Laursen, UAF. Spores of fungal species have been found in the feces that were not detected in field sampling by researchers (Laursen, pers. comm.). In this manner, the small mammal monitoring is also, indirectly, contributing to the monitoring of fungi in DNPP, while providing information on food habits of voles.

b. Detection of significant changes in small mammal populations

Determination of biologically significant changes in vole populations is still problematic after 5 years of data collection. Voles in the genus *Microtus* have not demonstrated strong abundance at any point during the 5 years of study. However, the populations do not appear to be in jeopardy, returning year after year. Northern red-backed voles have experienced dramatic fluctuations in population abundance (a six-fold change 1994-95). However, there is no clear pattern in abundance changes. Even low population sizes do not prevent red-backed voles from rebounding in subsequent years. I would speculate that 2 consecutive years of population abundance < 25 animals per plot at the end of the field season may be cause for concern.

Population survival rate is more problematic because in years of low population abundance, population survival rate is difficult to estimate because of lack of data. An additional complication is that apparent survival (product of surviving and not emigrating) is the parameter being estimated. Survival rate within a season on the order of 0.3 would seem difficult for population maintenance. Potentially the use of trends in survival rate over a number of seasons would be more indicative of population stress. Survival rates in this realm for 2 consecutive years would potentially necessitate research or management intervention.

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Appendix I. SAS code for generation of capture histories for analysis via CAPTURE.

```
**************************************************************************;
*        MAKEXMAT.SAS   ---  19 May 1991,  Eric Rexstad          ;
*                      22 May 1991 Modified age/sex specific ;
*  Converts raw data file into x-matrix for use in program CAPTURE   ;
*             Modified 27 August 1992 for ALASKA                ;
*             Modified 27 June 1995 for Denali grids & webs      ;
**************************************************************************;

**********************             User input required;
%let location = Den;        /*    Modify these 3 lines to     */
%let session = s1_96;
%let begdate = 1 July 1996;  /*    correspond with data set    */
%let occ = 15;              /*  being prepared for analysis.  */
**********************;

libname ses1 'c:\research\smalmam\denali\96\session1';
data; set ses1.s1sex;
  minute = 0;  second = 0;
  cattim = dhms(date2, hour, minute, second);
  keep date2 hour cattim x y tag sex plot spec wt;

proc sort; by cattim;
data days; set _last_; by cattim;
                /*  Determine number of days in trapping period */;
  if first.cattim then day+1;


                /*  Subset by plot or web */;
data fl; set days; if plot = 'FL';
data rl; set days; if plot = 'RL';
data fww; set days; if plot = 'FWW';
data fwe; set days; if plot = 'FWE';
data rw; set days; if plot = 'RW';

                /* Subset by spec and sex within plot */;

data clfl; set fl; if spec = 'CLRU'; run;
data mifl; set fl; if substr(spec,1,2) = 'MI'; run;
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```
proc sort data=clfl; by tag day;
proc sort data=mifl; by tag day;

data clrl; set rl; if spec = 'CLRU'; run;
data mirl; set rl; if substr(spec,1,2) = 'MI'; run;

proc sort data=clrl; by tag day;
proc sort data=mirl; by tag day;

data clfww; set fww; if spec = 'CLRU'; run;
data mifww; set fww; if substr(spec,1,2) = 'MI'; run;
proc sort data=clfww; by tag day;
proc sort data=mifww; by tag day;

data clfwe; set fwe; if spec = 'CLRU'; run;
data mifwe; set fwe; if substr(spec,1,2) = 'MI'; run;
proc sort data=clfwe; by tag day;
proc sort data=mifwe; by tag day;

data clrw; set rw; if spec = 'CLRU'; run;
data mirw; set rw; if substr(spec,1,2) = 'MI'; run;
proc sort data=clrw; by tag day;
proc sort data=mirw; by tag day;

*****************************************************;
/*       Process Forest Lower data                 */;
*****************************************************;

data sorted; set clfl end=last; by tag;
        /* Construct x-matrix (as array) for cleth  */;

 array xmat{&occ} x1-x&occ;
 retain x1-x&occ;
 file "&location&session..inp" mod;

 if _N_ = 1 then do;
  put "title='Site &location Lower Forest Cleth beginning &begdate'";
  put "task read captures occasions=&occ x matrix";
  put "format='(4x,a6,8x,20f1.0)'";
  put 'Read Input Data';
 end;

 if first.tag then do;
  do i=1 to dim(xmat);
   xmat{i} = 0;
```

```
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end;
run;

data sorted; set mifl end=last; by tag;
              /* Construct x-matrix (as array) for Microtus */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Lower Forest Microtus beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end; run;

*******************************************************;
/*     Process Lower Riparian data               */;
*******************************************************;

data sorted; set clrl end=last; by tag;
              /* Construct x-matrix (as array) for cleth */;
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```
  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Lower Riparian Cleth beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end;
run;

data sorted; set mirl end=last; by tag;
              /* Construct x-matrix (as array) for Microtus */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Lower Riparian Microtus beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
```

```
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end; run;

*************************************************************;
/*          Process Forest Web West data           */;
*************************************************************;

data sorted; set clfww end=last; by tag;
            /* Construct x-matrix (as array) for cleth */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Forest Web West Cleth beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end;
run;

data sorted; set mifww end=last; by tag;
            /* Construct x-matrix (as array) for Microtus */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;
```

```
  if _N_ = 1 then do;
    put "title='Site &location Forest Web West Microtus beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end; run;

/*          Data for input to DISTANCE              */;
data clfww1;  set clfww;  by tag;
  if first.tag then do;
    output;
  end;

title 'First captures of CLRU on FWW';
proc freq; tables x/norow nocol nopercent;
run;
/*          Trap occupancy                    */;
title 'Capture locations of Red-backs on FWW';
proc freq data=clfww; tables y*x/norow nocol nopercent;
run;

/*          Data for input to DISTANCE              */;
data mifww1;  set mifww; by tag;
  if first.tag then do;
     output;
  end;
title 'First captures of Microtus on FWW';
proc freq; tables x/norow nocol nopercent;
run;
/*          Trap occupancy                    */;
title 'Capture locations of Microtus on FWW';
proc freq data=mifww; tables y*x/norow nocol nopercent;
```

```
run;

***************************************************************;
/*          Process Forest Web East data             */;
***************************************************************;
data sorted; set clfwe end=last; by tag;
            /* Construct x-matrix (as array) for cleth */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Forest Web East Cleth beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end;
run;

data sorted; set mifwe end=last; by tag;
            /* Construct x-matrix (as array) for Microtus */;

  array xmat{&occ} x1-x&occ;
  retain x1-x&occ;
  file "&location&session..inp" mod;

  if _N_ = 1 then do;
    put "title='Site &location Forest Web East Microtus beginning &begdate'";
    put "task read captures occasions=&occ x matrix";
    put "format='(4x,a6,8x,20f1.0)'";
    put 'Read Input Data';
```

```
  end;

  if first.tag then do;
    do i=1 to dim(xmat);
      xmat{i} = 0;
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end; run;

/*        Data for input to DISTANCE             */;
data clfwe1;  set clfwe;  by tag;
  if first.tag then do;
    output;
  end;
run;
title 'First captures of CLRU on FWE';
proc freq; tables x/norow nocol nopercent;
run;
/*        Trap occupancy                  */;
title 'Capture locations of Red-backs on FWE';
proc freq data=clfwe; tables y*x/norow nocol nopercent;
run;

/*        Data for input to DISTANCE             */;
data mifwe1;  set mifwe; by tag;
  if first.tag then do;
     output;
  end;
run;
title 'First captures of Microtus on FWE';
proc freq; tables y/norow nocol nopercent;
run;
/*        Trap occupancy                  */;
title 'Capture locations of Microtus on FWW';
proc freq data=mifwe; tables y*x/norow nocol nopercent;run;

****************************************************************;
/*          Process Riparian Web data            */;
****************************************************************;
```

```
data sorted; set clrw end=last; by tag;
        /* Construct x-matrix (as array) for cleth */;

 array xmat{&occ} x1-x&occ;
 retain x1-x&occ;
 file "&location&session..inp" mod;

 if _N_ = 1 then do;
   put "title='Site &location Riparian Web Cleth beginning &begdate'";
   put "task read captures occasions=&occ x matrix";
   put "format='(4x,a6,8x,20f1.0)'";
   put 'Read Input Data';
 end;

 if first.tag then do;
   do i=1 to dim(xmat);
     xmat{i} = 0;
   end;
 end;
 xmat{day} = 1;
 if last.tag then put tag spec  sex (x1-x&occ) (1.);
 if last then do;
   put 'Task Model Selection';
   put 'Task Closure Test';
   put 'Task Population Estimate Appropriate';
 end;
run;

data sorted; set mirw end=last; by tag;
        /* Construct x-matrix (as array) for Microtus */;

 array xmat{&occ} x1-x&occ;
 retain x1-x&occ;
 file "&location&session..inp" mod;

 if _N_ = 1 then do;
   put "title='Site &location Riparian Web Microtus beginning &begdate'";
   put "task read captures occasions=&occ x matrix";
   put "format='(4x,a6,8x,20f1.0)'";
   put 'Read Input Data';
 end;

 if first.tag then do;
   do i=1 to dim(xmat);
     xmat{i} = 0;
```

```
    end;
  end;
  xmat{day} = 1;
  if last.tag then put tag spec  sex (x1-x&occ) (1.);
  if last then do;
    put 'Task Model Selection';
    put 'Task Closure Test';
    put 'Task Population Estimate Appropriate';
  end; run;

/*          Data for input to DISTANCE              */;
data clrw1;  set clrw;  by tag;
  if first.tag then do;
    output;
  end;
run;
title 'First captures of CLRU on RW';
proc freq; tables x/norow nocol nopercent;
run;
/*          Trap occupancy                          */;
title 'Capture locations of Red-backs on RW';
proc freq data=clrw; tables y*x/norow nocol nopercent;
run;

/*          Data for input to DISTANCE              */;
data mirw1;  set mirw; by tag;
  if first.tag then do;
     output;
  end;
run;
title 'First captures of Microtus on RW';
proc freq; tables x/norow nocol nopercent;
run;
/*          Trap occupancy                          */;
title 'Capture locations of Microtus on RW';
proc freq data=mirw; tables y*x/norow nocol nopercent;
run;

*****************************************************************;
/*          Trap occupancy for grids                */;
*****************************************************************;

/*            Process Riparian plot data            */;
title 'Capture locations of Red-backs on RL';
proc freq data=clrl; tables y*x/norow nocol nopercent;
```

```
run;

title 'Capture locations of Microtus on RL';
proc freq data=mirl; tables y*x/norow nocol nopercent;
run;

/*          Process Forest plot data            */;
title 'Capture locations of Red-backs on FL';
proc freq data=clfl; tables y*x/norow nocol nopercent;
run;

title 'Capture locations of Microtus on FL';
proc freq data=mifl; tables y*x/norow nocol nopercent;
run;

/*          Session check activity by plot, species     */;
title "Check activity &session for Clethrionomys";
title2 'Plot FL';
proc freq data=clfl; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot RL';
proc freq data=clrl; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot FWW';
proc freq data=clfww; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot FWE';
proc freq data=clfwe; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot RW';
proc freq data=clrw; tables date2*hour/norow nocol nopercent;
run;

title "Check activity &session for Microtus";
title2 'Plot FL';
proc freq data=mifl; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot RL';
proc freq data=mirl; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot FWW';
proc freq data=mifww; tables date2*hour/norow nocol nopercent;
run;
title2 'Plot FWE';
proc freq data=mifwe; tables date2*hour/norow nocol nopercent;
```

```
run;
title2 'Plot RW';
proc freq data=mirw; tables date2*hour/norow nocol nopercent;
run;
```